

IN THE CLAIMS:

Please cancel Claim 45 amend the Claims 42 and 43 as follows:

42. (Twice Amended) A method of determining a compound which alters the conductive property of an acetylcholine receptor, said acetylcholine receptor comprising a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO:1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40% identity to an amino acid sequence as set forth in SEQ ID NO:2 over its entire length

the method comprising:

culturing in the presence of the at least one compound a host cell stably transfected or transformed with a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO:1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40% identity to the amino acid sequence as set forth in SEQ ID NO: 2 over the entire length, and

detecting the altered conductive property of the receptor.

43. (Twice Amended) A method of determining a compound specifically binding to an acetylcholine receptor which compound upon binding alters the conductive property of the acetylcholine receptor, said acetylcholine receptor comprising a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO:1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40%

identity to the amino acid sequence as set forth in SEQ ID NO: 2 over the entire length,

the method comprising:

exposing a host cell stably transfected or transformed with a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO: 1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40% identity to the amino acid sequence as set forth in SEQ. ID NO: 2 over the entire length,

or

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exposing a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO: 1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40% identity to the amino acid sequence as set forth in SEQ. ID NO: 2 over the entire length,,

or

exposing an acetylcholine receptor comprising a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO: 1, sequences which, owing to the degeneracy of the genetic code, encode the same amino acid sequence as does the sequence as set forth in SEQ ID NO: 1, and sequences which encode a polypeptide having an amino acid sequence which has at least 40% identity to the amino acid sequence as set forth in SEQ. ID NO: 2 over the entire length,

to at least one compound under conditions permitting the interaction of the at least one compound with the host cell, the polypeptide or the receptor, and identifying the compound specifically binding to the receptor.